

SH3
Patent Application US/07/946,2361 SEQUENCE LISTING
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(1) GENERAL INFORMATION:

(i) APPLICANT: Jacobs, Cindy A.
Smith, Craig A.(ii) TITLE OF INVENTION: Method of Treating TNF-Dependent
Inflammation Using Tumor Necrosis Factor Antagonists

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Immunex Corporation
(B) STREET: 51 University Street
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: U.S.A.
(F) ZIP: 98101

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Wight, Christopher L.
(B) REGISTRATION NUMBER: 31,680
(C) REFERENCE/DOCKET NUMBER: 2503

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 587-0430
(B) TELEFAX: (206) 587-0606

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1641 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

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54
55 (iv) ANTI-SENSE: NO
56
57 (vi) ORIGINAL SOURCE:
58 (A) ORGANISM: Homo sapiens
59 (G) CELL TYPE: Fibroblast
60 (H) CELL LINE: WI-26 VA4
61
62 (vii) IMMEDIATE SOURCE:
63 (A) LIBRARY: WI-26 VA4
64 (B) CLONE: Clone 1
65
66 (ix) FEATURE:
67 (A) NAME/KEY: CDS
68 (B) LOCATION: 88..1473
69
70 (ix) FEATURE:
71 (A) NAME/KEY: mat_peptide
72 (B) LOCATION: 154..1470
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74 (ix) FEATURE:
75 (A) NAME/KEY: sig_peptide
76 (B) LOCATION: 88..153
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78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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80 GCGAGGCAGG CAGCCTGGAG AGAAGGCGCT GGGCTGCGAG GGCGCGAGGG CGCGAGGGCA 6
81
82 GGGGGCAACC GGACCCCGCC CGCATCC ATG GCG CCC GTC GCC GTC TGG GCC 11
83 Met Ala Pro Val Ala Val Trp Ala
84 -22 -20 -15
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86 GCG CTG GCC GTC GGA CTG GAG CTC TGG GCT GCG GCG CAC GCC TTG CCC 15
87 Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro
88 -10 -5 1
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90 GCC CAG GTG GCA TTT ACA CCC TAC GCT GCC CCG GAG CCC GGG AGC ACA TGC 20
91 Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
92 5 10 15
93
94 CCG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG ATG TGC TGC AGC AAA 25
95 Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
96 20 25 30
97
98 TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT ACC AAG ACC TCG GAC 30
99 Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp
100 35 40 45 50
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102 ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC ACC CAG CTC TGG AAC 35
103 Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn
104 55 60 65
105
106

107	TGG	GTT	CCC	GAG	TGC	TTG	AGC	TGT	GGC	TCC	CGC	TGT	AGC	TCT	GAC	CAG	39
108	Trp	Val	Pro	Glu	Cys	Leu	Ser	Cys	Gly	Ser	Arg	Cys	Ser	Ser	Asp	Gln	
109																80	
110																	
111	GTG	GAA	ACT	CAA	GCC	TGC	ACT	CGG	GAA	CAG	AAC	CGC	ATC	TGC	ACC	TGC	44
112	Val	Glu	Thr	Gln	Ala	Cys	Thr	Arg	Glu	Gln	Asn	Arg	Ile	Cys	Thr	Cys	
113																95	
114																	
115	AGG	CCC	GGC	TGG	TAC	TGC	GCG	CTG	AGC	AAG	CAG	GAG	GGG	TGC	CGG	CTG	49
116	Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Leu	Ser	Lys	Gln	Glu	Gly	Cys	Arg	Leu	
117																100	
118																105	
119	TGC	GCG	CCG	CTG	CGC	AAG	TGC	CGC	CCG	GGC	TTC	GGC	GTG	GCC	AGA	CCA	54
120	Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg	Pro	Gly	Phe	Gly	Val	Ala	Arg	Pro	
121																120	
122																125	
123	GGA	ACT	GAA	ACA	TCA	GAC	GTG	GTG	TGC	AAG	CCC	TGT	GCC	CCG	GGG	ACG	59
124	Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	Cys	Lys	Pro	Gly	Val	Ala	Arg	Pro	
125																135	
126																140	
127	TTC	TCC	AAC	ACG	ACT	TCA	TCC	ACG	GAT	ATT	TGC	AGG	CCC	CAC	CAG	ATC	63
128	Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	Asp	Ile	Cys	Arg	Pro	His	Gln	Ile	
129																150	
130																155	
131	TGT	AAC	GTG	GTG	GCC	ATC	CCT	GGG	AAT	GCA	AGC	ATG	GAT	GCA	GTC	TGC	68
132	Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	Asn	Ala	Ser	Met	Asp	Ala	Val	Cys	
133																165	
134																170	
135	ACG	TCC	ACG	TCC	CCC	ACC	CGG	AGT	ATG	GCC	CCA	GGG	GCA	GTA	CAC	TTA	73
136	Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	Met	Ala	Pro	Gly	Ala	Val	His	Leu	
137																180	
138																185	
139	CCC	CAG	CCA	GTG	TCC	ACA	CGA	TCC	CAA	CAC	ACG	CAG	CCA	ACT	CCA	GAA	78
140	Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	Gln	His	Thr	Gln	Pro	Thr	Pro	Glu	
141																195	
142																200	
143	CCC	AGC	ACT	GCT	CCA	AGC	ACC	TCC	TTC	CTG	CTC	CCA	ATG	GGC	CCC	AGC	83
144	Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser	Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser	
145																215	
146																220	
147	CCC	CCA	GCT	GAA	GGG	AGC	ACT	GGC	GAC	TTC	GCT	CTT	CCA	GTT	GGA	CTG	87
148	Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	Asp	Phe	Ala	Leu	Pro	Val	Gly	Leu	
149																230	
150																235	
151	ATT	GTG	GGT	GTG	ACA	GCC	TTG	GGT	CTA	CTA	ATA	ATA	GGA	GTG	GTG	AAC	92
152	Ile	Val	Gly	Val	Thr	Ala	Leu	Gly	Leu	Leu	Ile	Ile	Gly	Val	Val	Asn	
153																245	
154																250	
155	TGT	GTC	ATC	ATG	ACC	CAG	GTG	AAA	AAG	AAG	CCC	TTG	TGC	CTG	CAG	AGA	97
156	Cys	Val	Ile	Met	Thr	Gln	Val	Lys	Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg	
157																260	
158																265	
159	GAA	GCC	AAG	GTG	CCT	CAC	TTG	CCT	GCC	GAT	AAG	GCC	CGG	GGT	ACA	CAG	102

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160 Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln 161 275 280 285 290
162
163 GGC CCC GAG CAG CAG CAC CTG CTG ATC ACA GCG CCG AGC TCC AGC AGC 107
164 Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser Ser
165 295 300 305
166
167 AGC TCC CTG GAG AGC TCG GCC AGT GCG TTG GAC AGA AGG GCG CCC ACT 111
168 Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr
169 310 315 320
170
171 CGG AAC CAG CCA CAG GCA CCA GGC GTG GAG GCC AGT GGG GCC GGG GAG 116
172 Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu
173 325 330 335
174
175 GCC CGG GCC AGC ACC GGG AGC TCA GAT TCT TCC CCT GGT GGC CAT GGG 121
176 Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly
177 340 345 350
178
179 ACC CAG GTC AAT GTC ACC TGC ATC GTG AAC GTC TGT AGC AGC TCT GAC 126
180 Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp
181 355 360 365 370
182
183 CAC AGC TCA CAG TGC TCC TCC CAA GCC AGC TCC ACA ATG GGA GAC ACA 131
184 His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr
185 375 380 385
186
187 GAT TCC AGC CCC TCG GAG TCC CCG AAG GAC GAG CAG GTC CCC TTC TCC 135
188 Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val Pro Phe Ser
189 390 395 400
190
191 AAG GAG GAA TGT GCC TTT CGG TCA CAG CTG GAG ACG CCA GAG ACC CTG 140
192 Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro Glu Thr Leu
193 405 410 415
194
195 CTG GGG AGC ACC GAA GAG AAG CCC CTG CCC CTT GGA GTG CCT GAT GCT 145
196 Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala
197 420 425 430
198
199 GGG ATG AAG CCC AGT TAACCAGGCC GGTGTGGCT GTGTCGTAGC CAAGGTGGC 151
200 Gly Met Lys Pro Ser
201 435 440
202
203 TGAGCCCTGG CAGGATGACC CTGCGAAGGG GCCCTGGTCC TTCCAGGCC CCACCACTAG 157
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205 GACTCTGAGG CTCTTCTGG GCCAAGTTCC TCTAGTGCC TCCACAGCCG CAGCCTCCCT 163
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207 CTGACCTGCA G 164
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210 (2) INFORMATION FOR SEQ ID NO:2:
211
212 (i) SEQUENCE CHARACTERISTICS:

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213 (A) LENGTH: 461 amino acids
214 (B) TYPE: amino acid
215 (D) TOPOLOGY: linear
216
217 (ii) MOLECULE TYPE: protein
218
219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
220
221 Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
222 -22 -20 -15 -10
223
224 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
225 -5 1 5 10
226
227 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
228 15 20 25
229
230 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
231 30 35 40
232
233 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
234 45 50 55
235
236 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
237 60 65 70
238
239 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
240 75 80 85 90
241
242 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
243 95 100 105
244
245 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
246 110 115 120
247
248 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
249 125 130 135
250
251 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
252 140 145 150
253
254 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
255 155 160 165 170
256
257 Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
258 175 180 185
259
260 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
261 190 195 200
262
263 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
264 205 210 215
265

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266 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
267 220 225 230
268
269 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
270 235 240 245 250
271
272 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
273 255 260 265
274
275 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
276 270 275 280
277
278 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
279 285 290 295
280
281 Ile Thr Ala Pro Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
282 300 305 310
283
284 Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
285 315 320 325 330
286
287 Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
288 335 340 345
289
290 Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
291 350 355 360
292
293 Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
294 365 370 375
295
296 Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
297 380 385 390
298
299 Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
300 395 400 405 410
301
302 Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
303 415 420 425
304
305 Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
306 430 435
307
308
309 (2) INFORMATION FOR SEQ ID NO:3:
310
311 (i) SEQUENCE CHARACTERISTICS:
312 (A) LENGTH: 1557 base pairs
313 (B) TYPE: nucleic acid
314 (C) STRANDEDNESS: single
315 (D) TOPOLOGY: linear
316
317 (ii) MOLECULE TYPE: cDNA
318

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319 (iii) HYPOTHETICAL: NO
320
321 (iv) ANTI-SENSE: NO
322
323
324 (vii) IMMEDIATE SOURCE:
325 (B) CLONE: TNFR/Fc Fusion Protein
326
327 (ix) FEATURE:
328 (A) NAME/KEY: CDS
329 (B) LOCATION: 1..1557
330
331 (ix) FEATURE:
332 (A) NAME/KEY: mat_peptide
333 (B) LOCATION: 1..1554
334
335
336 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
337

338 GCG AGG CAG GCA GCC TGG AGA GAA GGC GCT GGG CTG CGA GGG CGC GAG 4
339 Ala Arg Gln Ala Ala Trp Arg Glu Gly Ala Gly Leu Arg Gly Arg Glu
340 1 5 10 15
341
342 GGC GCG AGG GCA GGG GGC AAC CGG ACC CCG CCC GCA TCC ATG GCG CCC 9
343 Gly Ala Arg Ala Gly Gly Asn Arg Thr Pro Pro Ala Ser Met Ala Pro
344 20 25 30
345
346 GTC GCC GTC TGG GCC GCG CTG GCC GTC GGA CTG GAG CTC TGG GCT GCG 14
347 Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala
348 35 40 45
349
350 GCG CAC GCC TTG CCC GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG 19
351 Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu
352 50 55 60
353
354 CCC GGG AGC ACA TGC CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG 24
355 Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln
356 65 70 75 80
357
358 ATG TGC TGC AGC AAA TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT 28
359 Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys
360 85 90 95
361
362 ACC AAG ACC TCG GAC ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC 33
363 Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr
364 100 105 110
365
366 ACC CAG CTC TGG AAC TGG GTT CCC GAG TGC TTG AGC TGT GGC TCC CGC 38
367 Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg
368 115 120 125
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370 TGT AGC TCT GAC CAG GTG GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC 43
371 Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn

372	130	135	140	
373				
374	CGC ATC TGC ACC TGC AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG			48
375	Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln			
376	145 150	155	160	
377				
378	GAG GGG TGC CGG CTG TGC GCG CCG CTG CGC AAG TGC CGC CCC GGC TTC			52
379	Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe			
380	165	170	175	
381				
382	GGC GTG GCC AGA CCA GGA ACT GAA ACA TCA GAC GTG GTG TGC AAG CCC			57
383	Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro			
384	180	185	190	
385				
386	TGT GCC CCG GGG ACG TTC TCC AAC ACG ACT TCA TCC ACG GAT ATT TGC			62
387	Cys Ala Pro Gly Thr Phe Ser Asn Thr Ser Ser Thr Asp Ile Cys			
388	195	200	205	
389				
390	AGG CCC CAC CAG ATC TGT AAC GTG GTG GCC ATC CCT GGG AAT GCA AGC			67
391	Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser			
392	210	215	220	
393				
394	ATG GAT GCA GTC TGC ACG TCC ACG TCC CCC ACC CGG AGT ATG GCC CCA			72
395	Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro			
396	225	230	235	240
397				
398	GGG GCA GTA CAC TTA CCC CAG CCA GTG TCC ACA CGA TCC CAA CAC ACG			76
399	Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr			
400	245	250	255	
401				
402	CAG CCA ACT CCA GAA CCC AGC ACT GCT CCA AGC ACC TCC TTC CTG CTC			81
403	Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu			
404	260	265	270	
405				
406	CCA ATG GGC CCC AGC CCC CCA GCT GAA GGG AGC ACT GGC GAC GAG CCC			86
407	Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Glu Pro			
408	275	280	285	
409				
410	AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA			91
411	Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu			
412	290	295	300	
413				
414	CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC			96
415	Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp			
416	305	310	315	320
417				
418	ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC			100
419	Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp			
420	325	330	335	
421				
422	GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC			105
423	Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly			
424	340	345	350	

425	GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC	110
426	Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn	
427	355 360 365	
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430	AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG	115
431	Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp	
432	370 375 380	
433		
434	CTG AAT GGC AAG GAC TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA	120
435	Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro	
436	385 390 395 400	
437		
438	GCC CCC ATG CAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA	124
439	Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu	
440	405 410 415	
441		
442	CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC	129
443	Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn	
444	420 425 430	
445		
446	CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGG CAC ATC	134
447	Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg His Ile	
448	435 440 445	
449		
450	GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC	139
451	Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr	
452	450 455 460	
453		
454	ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG	144
455	Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys	
456	465 470 475 480	
457		
458	CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC	148
459	Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys	
460	485 490 495	
461		
462	TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC	153
463	Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu	
464	500 505 510	
465		
466	TCC CTG TCT CCG GGT AAA TGA	15
467	Ser Leu Ser Pro Gly Lys	
468	515	
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470		
471	(2) INFORMATION FOR SEQ ID NO:4:	
472		
473	(i) SEQUENCE CHARACTERISTICS:	
474	(A) LENGTH: 518 amino acids	
475	(B) TYPE: amino acid	
476	(D) TOPOLOGY: linear	
477		

478 (ii) MOLECULE TYPE: protein
479
480 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
481
482 Ala Arg Gln Ala Ala Trp Arg Glu Gly Ala Gly Leu Arg Gly Arg Glu
483 1 5 10 15
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485 Gly Ala Arg Ala Gly Gly Asn Arg Thr Pro Pro Ala Ser Met Ala Pro
486 20 25 30
487
488 Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala
489 35 40 45
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491 Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu
492 50 55 60
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494 Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln
495 65 70 75 80
496
497 Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys
498 85 90 95
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500 Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr
501 100 105 110
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503 Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg
504 115 120 125
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506 Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn
507 130 135 140
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509 Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln
510 145 150 155 160
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512 Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe
513 165 170 175
514
515 Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro
516 180 185 190
517
518 Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys
519 195 200 205
520
521 Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser
522 210 215 220
523
524 Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro
525 225 230 235 240
526
527 Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr
528 245 250 255
529
530 Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu

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531 260 265 270
532
533 Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Glu Pro
534 275 280 285
535
536 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
537 290 295 300
538
539 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
540 305 310 315 320
541
542 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
543 325 330 335
544
545 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
546 340 345 350
547
548 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
549 355 360 365
550
551 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
552 370 375 380
553
554 Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
555 385 390 395 400
556
557 Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
558 405 410 415
559
560 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
561 420 425 430
562
563 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg His Ile
564 435 440 445
565
566 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
567 450 455 460
568
569 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
570 465 470 475 480
571
572 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
573 485 490 495
574
575 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
576 500 505 510
577
578 Ser Leu Ser Pro Gly Lys
579 515
580
581
582 (2) INFORMATION FOR SEQ ID NO:5:
583

Patent Application US/07/946,236

584 (i) SEQUENCE CHARACTERISTICS:
585 (A) LENGTH: 22 base pairs
586 (B) TYPE: nucleic acid
587 (C) STRANDEDNESS: single
588 (D) TOPOLOGY: linear
589
590 (ii) MOLECULE TYPE: DNA (genomic)
591
592 (iii) HYPOTHETICAL: NO
593
594 (iv) ANTI-SENSE: YES
595
596
597 (vii) IMMEDIATE SOURCE:
598 (B) CLONE: oligonucleotide
599
600
601 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
602
603 CGGTACGTGC TGTTGTTACT GC

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/946,236

DATE: 09/26/92
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SEQUENCE MISSING ITEM REPORT
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PRIOR APPLICATION DATA
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FILING DATE

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